

Copyright (C) 1993 - 2003	GenCore version 5.1.3	Compugen Ltd.
OM protein - protein search, using sw model		
Run on:	March 14, 2003, 05:19:53	Search time 1.04494 Seconds (without alignments)
Title:	US-09-698-781-17	827.996 Million cell updates/sec
Perfect score:	44	
Sequence:	1 TLFPVLLFL 9	
Scoring table:	BLOSUM62	
	Gapop 10.0	Gapext 0.5
Searched:	283224 seqs, 96134422 residues	
Total number of hits satisfying chosen parameters:	283224	
Minimum DB seq length:	0	
Maximum DB seq length:	200000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
	Listing first 45 summaries	
Database :	PIR 731*	
1:	pir1:*	
2:	pir2:*	
3:	pir3:*	
4:	pir4:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Score	Query Match Length DB ID
1	44	100.0 245 2 S68691
2	36	81.8 161 2 E8044
3	36	81.8 408 2 T39570
4	35	79.5 222 2 GT2297
5	35	79.5 227 2 F05624
6	35	79.5 361 2 D72384
7	35	79.5 543 2 E98939
8	35	79.5 1325 2 T0307
9	34	77.3 174 2 K70447
10	34	77.3 227 2 T11185
11	34	77.3 237 2 H84035
12	34	77.3 247 2 JE0307
13	34	77.3 301 1 S2864
14	34	77.3 330 1 T34250
15	34	77.3 356 2 G97072
16	34	77.3 405 2 B88976
17	34	77.3 511 2 A61912
18	34	77.3 653 2 G82971
19	34	77.3 741 2 T3086
20	33	75.0 89 2 B86833
21	33	75.0 303 2 A43708
22	33	75.0 350 2 DB8182
23	33	75.0 365 2 DT1559
24	33	75.0 365 2 B81713
25	33	75.0 459 2 A99392
26	33	75.0 483 2 G71523
27	33	75.0 668 2 E96777
28	33	75.0 744 2 T12705
29	33	75.0 1007 2 PNO156
RESULT 1		
S68691 neutrophil granules matrix glycoprotein SGP28 precursor - human		
C;Species: Homo sapiens (man)		
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000		
C;Accession: S68691; S74313; S68683		
R;Kjeldsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.		
FEBS Lett. 380, 246-250, 1996		
A;Title: SGP28, a novel matrix glycoprotein in specific granules of human neutrophil		
A;Reference number: S68691; MUID:96186934; PMID:8601434		
A;Molecule type: mRNA		
A;Residues: 1-245 <KIE>		
A;Cross-references: EMBL:X94323; PIDN:CAA63984.1; PID:91213613		
A;Molecule type: protein		
A;Residues: 33-83; 96-143; 165-217; 221-226 <KJL>		
A;Accession: S68691		
A;Molecule type: mRNA		
A;Residues: 1-245 <KIE>		
A;Cross-references: EMBL:X94313		
A;Molecule type: protein		
A;Accession: S68691; MUID:96270732; PMID:8665901		
A;Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure		
A;Reference number: S68681; MUID:96270732; PMID:8665901		
A;Accession: S68683		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-105; 'S', 107-245 <KRA>		
A;Cross-references: EMBL:X95240; MUID:91262818; PIDN:CAN64527.1; PID:91262819		
A;Genetics:		
A;GeneID: SGP28		
C;Superfamily: cysteine-rich secretory protein 1		
F1-19-20-245/Domain: signal sequence #status predicted <SIG>		
F1-19-20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted <M		
Query Match 100.0%; Score 44; DB 2; Length 245;		
Best Local Similarity 100.0%; pred 0.47; Mismatches 0; Indels 0; Gaps 0;		
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy 1 TLFPVLLFL 9		
Db 2 TLFPVLLFL 10		
RESULT 2		
E82044 ftsA protein VC2696 [imported] - Vibrio cholerae (strain N16961 serogroup 01)		
C;Species: Vibrio cholerae		
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001		
C;Accession: E82044		
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R		
I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.		
Nature 406, 477-483, 2000		
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.		

A; Reference number: A82035; MUID:20406833; PMID:10952301
 A; Accession: E82044
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-161 <HRI>
 A; Cross-references: GB:AE004335; GB:AE003852; NID:99657289; PIDN:AAF95837.1; GSPDB:GN001
 C; Genetics:
 A; Gene: VC696
 A; Map position: 1
 C; Superfamily: Escherichia coli hypothetical protein b4140
 Query Match^h
 Best Local Similarity 81.8%; Score 36; DB 2; Length 161;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVVLFL 9
 Db 1 MFPILLFL 8

RESULT 3
 T39570 probable metal transporter - fission yeast (*Schizosaccharomyces pombe*)
 C; Species: *Schizosaccharomyces pombe*
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
 C; Accession: T39570
 R; Wood, V.; Rolandream, M.A.; Barrell, B.G.; Brown, D.; Churcher, C.M.
 Submitted to the EMBL Data Library, March 1999
 A; Reference number: 221864
 A; Accession: T39570
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-408 <HPO>
 A; Cross-references: EMBL:AL035637; PIDN: CAB39510.1; GSPDB:GN00067; SPDB:SPBC16D10.06
 C; Genetics:
 A; Gene: SDDB:SPBC16D10.06
 A; Map position: 2

Query Match^h
 Best Local Similarity 81.8%; Score 36; DB 2; Length 408;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLFPVILF 8
 Db 281 TLFPVILF 288

RESULT 4
 G72297 conserved hypothetical protein - *Thermotoga maritima* (strain MSB8)
 C; Species: *Thermotoga maritima*
 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C; Accession: G72297
 R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, C.M.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
 Nature 399, 323-329, 1999
 A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A; Reference number: A72200; MUID:99287316; PMID:10360571
 A; Accession: D72384
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-361 <HRI>
 A; Cross-references: GB:AE001718; GB:AE000512; NID:94980881; PIDN:AAD35473.1; PID:9491
 A; Experimental source: strain MSB8
 C; Genetics:
 A; Gene: TM0388

Query Match^h
 Best Local Similarity 79.5%; Score 35; DB 2; Length 361;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVVLFL 9
 Db 25 LFPILLFL 32

RESULT 7
 E89839 Query Match^h
 Best Local Similarity 79.5%; Score 35; DB 2; Length 222;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 C; Genetics:
 A; Gene: TM1087
 C; Species: *Staphylococcus aureus* hypothetical protein SA0639 [imported] - *Staphylococcus aureus* (strain N315)
 C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C; Accession: E89839

RESULT 5
 F90624 ATP synthase F0 chain 6 [imported] - *Casuarinus casuarinus* mitochondrion
 C; Species: mitochondrion *Casuarinus casuarinus*
 C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 03-Aug-2001
 C; Accession: F90624
 R; Hadzirath, O.; Baker, A.J.
 Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001
 A; Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogeny
 A; Reference number: A99613; MUID:21263106; PMID:11370967
 A; Accession: F90624
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-227 <KUR>
 A; Cross-references: GB:NC_002778; NID:914141864; PIDN:NP_115355.1; GSPDB:GN00162
 C; Genetics:
 A; Gene: ATP6
 A; Genome: mitochondrion
 A; Genetic code: SGCI
 C; Superfamily: H+-transporting ATP synthase protein 6
 C; Keywords: mitochondrion
 Query Match^h
 Best Local Similarity 79.5%; Score 35; DB 2; Length 227;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVVLFL 8
 Db 25 LFPVILF 31

RESULT 6
 D72384 conserved hypothetical protein - *Thermotoga maritima* (strain MSB8)
 C; Species: *Thermotoga maritima*
 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C; Accession: D72384
 R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, C.M.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
 Nature 399, 323-329, 1999
 A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A; Reference number: A72200; MUID:99287316; PMID:10360571
 A; Accession: D72384
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-361 <HRI>
 A; Cross-references: GB:AE001718; GB:AE000512; NID:94980881; PIDN:AAD35473.1; PID:9491
 A; Experimental source: strain MSB8
 C; Genetics:
 A; Gene: TM0388

Query Match^h
 Best Local Similarity 79.5%; Score 35; DB 2; Length 361;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVVLFL 9
 Db 25 LFPILLFL 32

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C;Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet, 357, 1225-1240, 2001
A;Reference: Whole genome sequencing of meticillin-resistant staphylococcus aureus.
A;Accession: EG9839
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-543 <UR>
A;Cross-references: GB:BA000018; PID:913700575; PIDN:BA841872.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0639

RESULT 8
T01037 hypothetical protein YUP8H12R_20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999
C;Accession: T01037
R;Theologis, A.; Vysotskaya, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan, Oefner, P.; Davis, R.W.
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
A;Accession number: 214227
A;Status: translated from GB/EMBL/DDJB
A;Residues: 1-1325 <THE>
A;Cross-references: EMBL:AC002986; NID:92494106; PID:93152582; GSPDB:GN00059; RTSP:YUP8H
C;Genetics:
A;Gene: RTSP:YUP8H12R_20
A;Map position: 1
A;Introns: 70/2; 130/3; 233/3; 384/3; 450/3; 470/1; 687/3; 740/3; 765/3; 868/3; 940/3; 1
Query Match 79.5%; Score 35; DB 2; Length 543;
Best Local Similarity 75.0%; Pred. No. 53; Mismatches 6; Conservative 2; Indels 0; Gaps 0;
Matches 6; Mismatches 0; Indels 0; Gaps 0;
Oy 2 LFPVLLFL 9
Db 13 LFPVLMFL 20

RESULT 9
T01037 hypothetical protein aq_1706 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
C;Accession: AY0447
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'Neil, V.; Nature, 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: AY0300; MUID:98196666; PMID:9537320
A;Accession: AY0447
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-174 <AOF>
A;Cross-references: GB:AE000752; NID:92984021; PIDN:AC07575.1; PID:92984033; GB:AE00065
C;Genetics:
A;Gene: aq_1706

RESULT 10
T11185 H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - Smithornis sharpei mitoc
C;Species: mitochondrion Smithornis sharpei
C;Accession: T11185
R;Mindell, D.P.; Sorenson, M.D.; Blench, D.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 10693-10697, 1998
A;Title: Multiple independent origins of mitochondrial gene order in birds.
A;Reference number: Z17242
A;Accession: T11185
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Cross-references: EMBL:AF090340; NID:94894488; PID:94894494; PIDN:AD32519.1
A;Residues: 1-227 <MIN>
C;Genetics:
A;Gene: mitochondrion
A;Molecule type: DNA
A;Cross-references: EMBL:AF090340; NID:94894488; PID:94894494; PIDN:AD32519.1
A;Residues: 1-227 <MIN>
C;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
Query Match 77.3%; Score 34; DB 2; Length 227;
Best Local Similarity 75.0%; Pred. No. 35; Mismatches 6; Conservative 2; Indels 0; Gaps 0;
Matches 6; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TLFPVLLF 8
Db 24 TLFPMLY 31

RESULT 11
H84035 hypothetical protein BH3008 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Accession: H84035
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
R;Takami, H.; Nakagawa, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84035
A;Status: preliminary
A;Cross-references: GB:AP001517; GB:BA000004; NID:91017550; PIDN:BA806807.1; GSPDB:
C;Genetics:
A;Gene: BH3008
C;Superfamily: Bacillus subtilis hypothetical protein yoaT
Query Match 77.3%; Score 34; DB 2; Length 237;
Best Local Similarity 75.0%; Pred. No. 37; Mismatches 6; Conservative 2; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 2 LFPVLLFL 9
Db 16 LFPVVF 23

RESULT 12
JB0307 membrane protein - rat
A;Gene: aq_1706

C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
 C;Accession: JE0307
 R;Nakadal, T.; Kishimoto, T.; Kokura, K.; Okawa, N.; Makino, Y.; Muramatsu, M.; Tamura, DNA Res. 5, 315-317, 1998
 A;Title: Cloning of a novel rat gene, DB83, that encodes a putative membrane protein.
 A;Reference number: JE0307; MUID:99087491; PMID:9872456
 A;Accession: JE0307
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-247 <HAR>
 A;Cross-references: DDBJ:AB006135

Query Match 77.3%; Score 34; DB 2; Length 247;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TLFPVLF 8
 Db 111 SIFPVLLF 118

RESULT 13

S12864 retinal isomerase (EC 5.2.1.3) [validated] - Japanese flying squid

N;Alternate names: retinohchrome

C;Species: *Todirodes pacificus* (Japanese flying squid)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 01-Sep-2000

C;Accession: S12864; S39449

R;Hara-Nishimura, I.; Matsumoto, T.; Mori, H.; Nishimura, M.; Hara, R.; Hara, T.

FEBs Lett. 271, 106-110, 1990

A;Title: Cloning and nucleotide sequence of cDNA for retinohrome, retinal photoisomers

A;Reference number: S12864; MUID:91032043; PMID:2226795

A;Accession: S12864

A;Molecule type: mRNA

A;Residues: 1-301 <HAR>

A;Cross-references: EMBL:X57143; NID:910776; PID:910777

R;Hara-Nishimura, I.; Kondo, M.; Nishimura, M.; Hara, R.; Hara, T.

PEBS Lett. 335, 94-98, 1993

A;Title: Amino acid sequence surrounding the retinal-binding site in retinohrome of the

A;Reference number: S39449; MUID:94063090; PMID:8243675

A;Accession: S39449

A;Status: preliminary

A;Molecule type: protein

A;Residues: 274-277, 'X', 279-282 <HA2>

C;Superfamily: vertebrate rhodopsin

C;Keywords: chromoprotein; cis-trans-isomerase; G protein-coupled receptor; glycoprotein

C;1-301/Product: retinal isomerase #status experimental <MAT>

F;19-43/domain: transmembrane #status predicted <TM1>

F;54-75/domain: transmembrane #status predicted <TM2>

F;133-153/domain: transmembrane #status predicted <TM3>

F;181-208/domain: transmembrane #status predicted <TM4>

F;231-255/domain: transmembrane #status predicted <TM5>

F;265-288/domain: transmembrane #status predicted <TM6>

F;170/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;275/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 77.3%; Score 34; DB 1; Length 301;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFPVLF 9
 Db 280 LFPVLF 287

RESULT 14

T34250

hypothetical protein F31D5.6 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Accession: T34250

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

A;Map Position: 2

A;Introns: 28/2; 45/1; 79/2; 158/1; 223/3; 281/2

Query Match 77.3%; Score 34; DB 2; Length 330;
 Best Local Similarity 77.8%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLFPVLF 9
 Db 211 TFPVLF 219

R;Wilcox, L. submitted to the EMBL Data Library, June 1995

A;Description: The sequence of *C. elegans* cosmid F31D5.

R;Reference number: Z21194

A;Accession: T34250

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-330 <TLF>

A;Cross-references: EMBL:U28941; PIDN:AC71104.1; GSPDB:GN00020; CESP:F31D5.6

A;Experimental source: strain Bristol N2; clone F31D5

A;Genetics:

A;Gene: CESP:F31D5.6

A;Map Position: 2

A;Introns: 28/2; 45/1; 79/2; 158/1; 223/3; 281/2

Query Match 77.3%; Score 34; DB 2; Length 356;

Best Local Similarity 85.7%; Pred. No. 54;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFPVLF 8
 Db 23 LFPVLF 29

Search completed: March 14, 2003, 05:41:35

Job time : 4.04494 secs